

IN THE FIGURES:

Please replace Figures 3A-B, 6, 7A-B, and 8 with the revised Figures 3A-D, 6, 7A-D, and 8 attached herewith.



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9	18	27	36	45	54	
CTC	GAG	ATG	CAG	AGG	AAC	CTG
GGA	GCT	GTG	CTG	GGG	ATT	CTG
TGG	GTG	CAG	ATT	[SEQ ID NO: 1]		

L	E	M	Q	R	N	L
G	A	V	L	G	I	L
W	V	Q	I	[SEQ ID NO: 2]		

63	72	81	90	99	108	
TGC	TGG	CTG	AAA	GAA	CAG	CAA
GTG	CAG	CAG	AGT	CCC	GCA	TCC
TTG	GTT	CTG	CAG			

C	W	L	K	E	Q	Q
V	Q	Q	S	P	A	S
L	V	L	Q			

117	126	135	144	153	162	
GAG	GGG	GAG	AAC	GCA	GAG	CTC
CAG	TGT	AGC	TTT	TCC	ATC	TTT
ACA	AAC	CAG	GTG			

E	G	E	N	A	E	L
Q	C	S	F	S	I	F
T	N	Q	V			

171	180	189	198	207	216	
CAG	TGG	TTT	TAC	CAA	CGT	CCT
GGG	GGA	AGA	CTC	GTC	AGC	CTG
TTG	TAC	AAT	CCT			

Q	W	F	Y	Q	R	P
G	G	R	L	V	S	L
L	Y	N	P			

225	234	243	252	261	270	
TCT	GGG	ACA	AAG	CAG	AGT	GGG
AGA	CTG	ACA	TCC	ACA	ACA	GTC
ATT	AAA	GAA	CGT			

S	G	T	K	Q	S	G
R	L	T	S	T	T	V
I	K	E	R			

279	288	297	306	315	324	
CGC	AGC	TCT	TTG	CAC	ATT	TCC
TCC	TCC	CAG	ATC	ACA	GAC	TCA
GGC	ACT	TAT	CTC			

R	S	S	L	H	I	S
S	S	Q	I	T	D	S
G	T	Y	L			

FIG. 3A



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333	342	351	360	369	378
TGT GCC TCA AAT TCT	GGA GGA AGC AAT	GCA AAG CTA ACC	TTC GGG AAA GGC	ACT	
C A S N S	G G S N A	K L T F	G K G	T	
387	396	405	414	423	432
AAA CTC TCT GTT AAA	TCA GGT GGC GGA	GGG TCT GGC	GGG GGT GGA	TCC GGG GGT	
K L S V K	S G G G S	G G G G	S G S	G G	
441	450	459	468	477	486
GGA GGC TCA GAG GCT	GCA GTC ACC CAA	AGC CCA AGA	AAC AAG GTG	GCA GTA ACA	
G G S E A	A V T Q S	P R N K	V A V	T	
495	504	513	522	531	540
GGA GGA AAG GTG ACA	TTG AGC TGT AAT	CAG ACT AAT	AAC CAC AAC	AAC ATG TAC	
G G K V T	L S C N Q	T N N H	N N M	Y	
549	558	567	576	585	594
TGG TAT CGG CAG GAC	ACG GGG CAT GGG	CTG AGG CTG	ATC CAT TAT	TCA TAT GGT	
W Y R Q D	T G H G	L R L	I H Y	S Y G	
603	612	621	630	639	648
GCT GGC AGC ACT GAG	AAA GGA GAT ATC	CCT GAT GGA	TAC AAG GCC	TCC AGA CCA	
A G S T E	K G D I	P D G	Y K A	S R P	

FIG. 3B



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657	666	675	684	693	702
AGC CAA GAG AAC TTC TCC CTC ATT CTG GAG TTG GCT ACC CCC TCT CAG ACA TCA					

S	Q	E	N	F	S
L	I	L	E	L	A
T	P	S	Q	T	S

711	720	729	738	747	756
GTG TAC TTC TGT GCC AGC GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT					

V	Y	F	C	A	S
G	E	T	G	T	N
E	R	L	F	F	G

765	774	783	792	801	810
CAT GGA ACC AAG CTG TCT GTC CTG ACT AGT AAC TCC ATC ATG TAC TTC AGC CAC					

H	G	T	K	L	S
V	L	T	S	N	S
I	M	Y	F	S	H

819	828	837	846	855	864
TTC GTG CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG CCA GCG CCG CGA CCA					

F	V	P	V	F	L
P	A	K	P	T	T
T	T	P	A	P	R
P					

873	882	891	900	909	918
CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CCA TCT AGT					

P	T	P	A	P	T
I	A	S	Q	P	L
S	L	R	P	S	S

927	936	945	954	963	972
TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC TTC ATC TAT GGT					

S	R	D	P	K	L
C	Y	L	L	D	G
I	L	F	I	Y	G

FIG. 3C



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981	990	999	1008	1017	1026
GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC AGC AGG AGC GCA GAC GCC					

V	I	L	T	A	L
F	L	R	V	K	F
S	R	S	A	D	A
1035	1044	1053	1062	1071	1080
CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC TAT AAC GAG CTC AAT CTA GGA CGA					

P	A	Y	Q	Q	G
Q	N	Q	L	Y	N
E	L	N	L	G	R
1089	1098	1107	1116	1125	1134
AGA GAG GAG TAC GAT GTT TTG GAC AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG					

R	E	E	Y	D	V
L	D	K	R	R	G
R	D	P	E	M	G
1143	1152	1161	1170	1179	1188
GGA AAG CCG AGA AGG AAG AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA					

G	K	P	R	R	K
N	P	Q	E	G	L
Y	N	E	L	Q	K
1197	1206	1215	1224	1233	1242
GAT AAG ATG GCG GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG					

D	K	M	A	E	A
Y	S	E	I	G	M
K	G	E	R	R	R
1251	1260	1269	1278	1287	1296
GGC AAG GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GCC ACC AAG GAC ACC					

G	K	G	H	D	G
L	Y	Q	G	L	S
T	A	T	K	D	T
1305	1314	1323	1332		
TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAA					

Y	D	A	L	H	M
Q	A	L	P	P	R

FIG. 3D



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9	18	27	36	45	54	
ATG	AAA	TCC	TTG	AGT	GTT	TCC
CTA	GTG	GTC	CTG	TGG	CTC	CAG
TTA	AAC	TGG	GTG			
[SEQ ID NO: 43]						

Met	Lys	Ser	Leu	Ser	Val	Ser
Leu	Val	Val	Leu	Trp	Leu	Gln
Leu	Asn	Trp	Val			
[SEQ ID NO: 44]						

63	72	81	90	99	108	
CAG	AGC	CAG	CAG	AAG	GTG	CAG
CAG	AGC	CCA	GAA	TCC	CTC	AGT
GTC	CCA	GAG	GGA			

Gln	Ser	Gln	Gln	Lys	Val	Gln
Gln	Ser	Pro	Glu	Ser	Leu	Ser
Val	Pro	Glu	Gly			

117	126	135	144	153	162	
GGC	ATG	GCC	TCT	CTC	AAC	TGC
ACT	TCA	AGT	GAT	CGC	AAT	TTT
CAG	TAT	TTC	TGG			

Gly	Met	Ala	Ser	Leu	Asn	Cys
Thr	Ser	Ser	Asp	Arg	Asn	Phe
Gln	Tyr	Phe	Trp			

171	180	189	198	207	216	
TGG	TAC	AGA	CAG	CAT	TCT	GGA
GAA	GGC	CCC	AAA	GCA	CTG	ATG
TCC	ATC	TTC	TCT			

Trp	Tyr	Arg	Gln	His	Ser	Gly
Glu	Gly	Pro	Lys	Ala	Leu	Met
Ser	Ile	Phe	Ser			

FIG. 7A



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225	234	243	252	261	270												
GAT	GGT	GAC	AAG	AAA	GAA	GGC	AGA	TTC	ACA	GCT	CAC	CTC	AAT	AAG	GCC	AGC	CTG

Asp	Gly	Asp	Lys	Lys	Glu	Gly	Arg	Phe	Thr	Ala	His	Leu	Asn	Lys	Ala	Ser	Leu
279	288	297	306	315	324												
CAT	GTT	TCC	CTG	CAC	ATC	AGA	GAC	TCC	CAG	CCC	AGT	GAC	TCC	GCT	CTC	TAC	TTC

His	Val	Ser	Leu	His	Ile	Arg	Asp	Ser	Gln	Pro	Ser	Asp	Ser	Ala	Leu	Tyr	Phe
333	342	351	360	369	378												
TGT	GCA	GTT	ATG	GAT	TAT	AAC	CAG	GGG	AAG	CTT	ATC	TTT	GGG	CAG	GGT	ACC	AAG

Cys	Ala	Val	Met	Asp	Tyr	Asn	Gln	Gly	Lys	Leu	Ile	Phe	Gly	Gln	Gly	Thr	Lys
387																	
TTA	TCT	ATC	AAG	CCC	3'												

Leu	Ser	Ile	Lys	Pro													

FIG. 7B



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9	18	27	36	45	54	
ATG	GGC	TCC	AGA	CTC	TTC	TTT
GTG	GTT	TTG	ATT	CTC	CTG	TGT
GCA	AAA	CAC	ATG			
[SEQ ID NO: 45]						

Met	Gly	Ser	Arg	Leu	Phe	Phe
Val	Val	Leu	Ile	Leu	Leu	Cys
Ala	Lys	His	Met			
[SEQ ID NO: 46]						

63	72	81	90	99	108	
GAG	GCT	GCA	GTC	ACC	CAA	AGT
CCA	AGA	AGC	AAG	GTG	GCA	GTA
ACA	GGA	GGA	AAG			

Glu	Ala	Ala	Val	Thr	Gln	Ser
Pro	Arg	Ser	Lys	Val	Ala	Val
Thr	Gly	Gly	Lys			

117	126	135	144	153	162	
GTG	ACA	TTG	AGC	TGT	CAC	CAG
ACT	AAT	AAC	CAT	GAC	TAT	ATG
TAC	TGG	TAT	CGG			

Val	Thr	Leu	Ser	Cys	His	Gln
Thr	Asn	Asn	His	Asp	Tyr	Met
Tyr	Trp	Tyr	Arg			

171	180	189	198	207	216	
CAG	GAC	ACG	GGG	CAT	GGG	CTG
AGG	CTG	ATC	CAT	TAC	TCA	TAT
GTC	GCT	GAC	AGC			

Gln	Asp	Thr	Gly	His	Gly	Leu
Arg	Leu	Ile	His	Tyr	Ser	Tyr
Val	Ala	Asp	Ser			

FIG. 7C



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225	234	243	252	261	270
ACG GAG AAA GGA GAT ATC CCT GAT GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG					
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Thr Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu					
279	288	297	306	315	324
AAT TTC TCT CTC ATT CTG GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC					
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Asn Phe Ser Leu Ile Leu Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe					
333	342	351	360	369	378
TGT GCC AGC AGC GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT					
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Cys Ala Ser Ser Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly					
387	396				
CCC GGC ACC AGG CTC ACG GTT TCT 3'					
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Pro Gly Thr Arg Leu Thr Val Ser					

FIG. 7D



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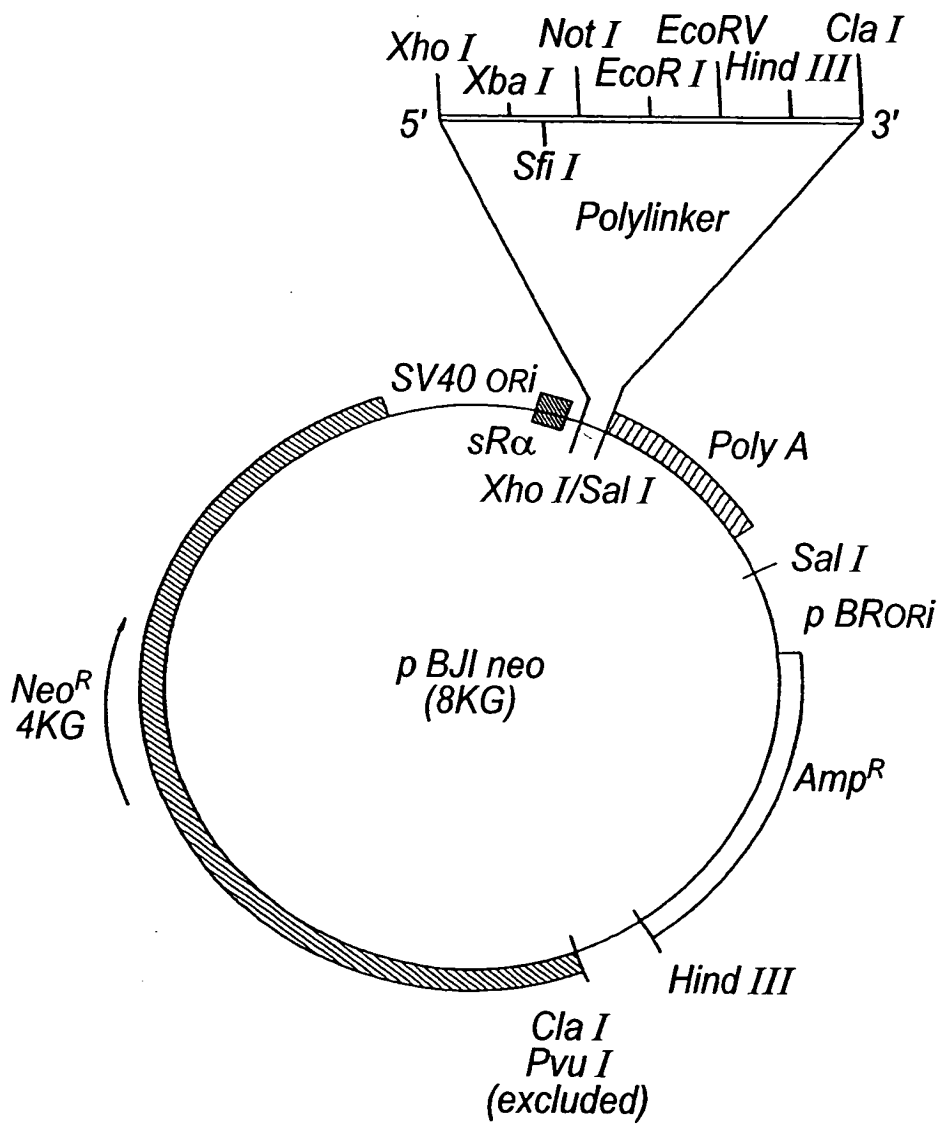


FIG. 8